



1600

## RAW SEQUENCE LISTING

DATE: 10/17/2002

PATENT APPLICATION: US/08/753,750B

TIME: 10:12:36

Input Set : A:\08753750 seqlisting.txt

Output Set: N:\CRF4\10172002\H753750B.raw

RECEIVED

OCT 30 2002

TECH CENTER 1600/2900

4 <110> APPLICANT: Lo, Reggie Y.C.  
 5 Schryvers, Anthony B.  
 6 Potter, Andrew A.  
 8 <120> TITLE OF INVENTION: TRANSFERRIN BINDING PROTEINS OF  
 9 PASTEURILLA HAEMOLYTICA AND VACCINES CONTAINING THE SAME  
 12 <130> FILE REFERENCE: A34762 021645.0105  
 C--> 14 <140> CURRENT APPLICATION NUMBER: US/08/753,750B  
 15 <141> CURRENT FILING DATE: 1996-11-29  
 17 <150> PRIOR APPLICATION NUMBER: CA 2,164,274  
 18 <151> PRIOR FILING DATE: 1995-12-01  
 20 <150> PRIOR APPLICATION NUMBER: 60/008,569  
 21 <151> PRIOR FILING DATE: 1995-12-01  
 23 <160> NUMBER OF SEQ ID NOS: 68  
 25 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
 27 <210> SEQ ID NO: 1  
 28 <211> LENGTH: 2793  
 29 <212> TYPE: DNA  
 30 <213> ORGANISM: Pasteurella haemolytica  
 32 <220> FEATURE:  
 33 <221> NAME/KEY: misc\_feature  
 34 <222> LOCATION: 2544  
 35 <223> OTHER INFORMATION: a, c, g or t  
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 39 cttttctcatt catacgggtgc tgcgactgaa aataaaaaaa tcgaagaaaa taacgatcta 120  
 40 gctgtttctgg atgaagttat tgtgacagag agccattatg ctcacgaacg tcaaaacgaa 180  
 41 gtaactggct tggggaaagt agtgaaaaat tatcacgaaa tgagtaaaaa tcaaattctt 240  
 42 ggtattcgtg atttaactcg ctatgaccct ggtatttcgg tgggtggaaca aggtcgcggt 300  
 43 gcaagtagtg gctatgccat tcgagggtgta gataaaaacc gtgtcagctt acttggtgat 360  
 44 gggctaccac aagcgcacag ttatcatacg ctagggttcag atgctaattg tgggtgcaatt 420  
 45 aatgagattg agtatgaaaa cattcgttca attgagttaa gcaaaggagc aagttctgcg 480  
 46 gaatatggct ctggtgcgca tgggtggtgct attgggtttc gtactaaaga tgcgcaggat 540  
 47 attattaaag aggggcagca ttggggccta gatagtaaga cctcttatgc cagcaaaaaat 600  
 48 agccattttt tacagtctat cgcagcggct ggtgaggcgg gtggttttga agcatttggt 660  
 49 attgcaactc accgacacgg taaagagacc aaaattcatt ccgaggcaaa taaattaaaa 720  
 50 cataatatte ggcgtataac cggctttgaa aatcgctacg actttaccca aattccgcac 780  
 51 agaatgctcc tggaggatct ccttttaatt gtggaagata cttgcccac attagattgt 840  
 52 actcctcgtg caagggttaa gttgaaccgc gataatttcc cagtgagaac atttccggaa 900  
 53 tatacgctg aagagcgcaa acagcttgag cagattcctt atcgcactga gcagctctca 960  
 54 gcccaagaat ataccggtaa agatcgcatt gcaccaaac ctttagatta caagagtaat 1020  
 55 tctgttttta tgaagtttgg ctatcacttc aactcgtctc attatcttgg cgcaatttta 1080  
 56 gaagatacaa aaacacgcta cgatatccgt gatatgcaaa cgccagctta ctatacaaaa 1140  
 57 gacgatatta acttatcact taggaactat gtttatgaag gggataatat tttagatggc 1200

ENTERED

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58 ttagtggttca agccaaggat cccttatggg ttgcgctata gccatgtgaa gttttttgat 1260
59 gaacgtcacc acaaacgtcg tttaggattc acctataaat ataaaccaga gaataatcgc 1320
60 tggttggata gcattaaact cagtgcggat aaacaagata ttgaactata tagccggcta 1380
61 catcgcttgc attgtagcga ttatcctgtg gtagataaaa attgccgccc gactttggat 1440
62 aaatcttggg ctatgtatcg aactgagcgt aataattacc aagaaaagca tcgtgtcatt 1500
63 catttagaat ttgataaagc gctaaatgct ggtcaaggcg tatttaacca aaccacaaa 1560
64 ctgaatttag ggttgggctt tgatcgattt aattcgctta tggatcatgg ggatatgact 1620
65 gcccaatata ccaaaggcgg ttataaccagc taccgcggta gagggcggtt agataatcca 1680
66 tatattttatc gccgcgatcc acgcagtatt gaaacgggtat ctttgtgtaa taatacacgc 1740
67 ggcgacatct taaactgtga accgcgtaaa attaaaggcg atagccattt tgtagcttc 1800
68 cgcgatctag tgataagcga gtatgtggat ttgggattag ggggtgcgtt tgatcaacat 1860
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70 ggtgggatta cgcttaaac aacagagttt gtatcgctt cttatcgcat ttcaaacggt 1980
71 tttagagtgc ctgcattcta tgaactttat ggtaaactgt atcatattgg gcttaaagat 2040
72 aacgaatatg tgcaacgcgc gcaacgtagc caccagttag agccagaaaa atcgactaat 2100
73 catgagattg gagtttagctt taaagggtcaa tttggttacc ttgatgtgag ctatttccgt 2160
74 aataactata aaaatatgat tgcgacagca tgtaaaagaa taatacaaaa atcacactgt 2220
75 ttctataact accataatat tcaagatgta gcactaaacg ggataaattt agtcgctaaa 2280
76 tttgacttac acggtatttt atctatgctg ccagatgggt tttattcatc agttgcttat 2340
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79 gaagaaaaat ggggaattgg cattactacc acctattcta aagccaaaaa cgccgatgag 2520
W--> 80 gtggcaggca cacgtcatca cggnatatc cgcgttgatt taggtggcaa actgaccggt 2580
81 tcttgggtaca cccatgatat taccggttac atcaattata aaaactacac cttacgtgga 2640
82 ggaatttata atgtgactaa tcgtaaatat tccacttggg aatcagtgcg ccaatccggt 2700
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87 <211> LENGTH: 930
88 <212> TYPE: PRT
89 <213> ORGANISM: Pasteurella haemolytica
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93 1 5 10 15
94 Val Leu Phe Ala Leu Ser His Ser Tyr Gly Ala Ala Thr Glu Asn Lys
95 20 25 30
96 Lys Ile Glu Glu Asn Asn Asp Leu Ala Val Leu Asp Glu Val Ile Val
97 35 40 45
98 Thr Glu Ser His Tyr Ala His Glu Arg Gln Asn Glu Val Thr Gly Leu
99 50 55 60
100 Gly Lys Val Val Lys Asn Tyr His Glu Met Ser Lys Asn Gln Ile Leu
101 65 70 75 80
102 Gly Ile Arg Asp Leu Thr Arg Tyr Asp Pro Gly Ile Ser Val Val Glu
103 85 90 95
104 Gln Gly Arg Gly Ala Ser Ser Gly Tyr Ala Ile Arg Gly Val Asp Lys
105 100 105 110
106 Asn Arg Val Ser Leu Leu Val Asp Gly Leu Pro Gln Ala His Ser Tyr
107 115 120 125
108 His Thr Leu Gly Ser Asp Ala Asn Gly Gly Ala Ile Asn Glu Ile Glu

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109	130	135	140
110	Tyr Glu Asn Ile Arg Ser Ile Glu Leu Ser Lys Gly Ala Ser Ser Ala		
111	145	150	155
112	Glu Tyr Gly Ser Gly Ala His Gly Gly Ala Ile Gly Phe Arg Thr Lys		
113		165	170
114	Asp Ala Gln Asp Ile Ile Lys Glu Gly Gln His Trp Gly Leu Asp Ser		
115		180	185
116	Lys Thr Ser Tyr Ala Ser Lys Asn Ser His Phe Leu Gln Ser Ile Ala		
117		195	200
118	Ala Ala Gly Glu Ala Gly Gly Phe Glu Ala Leu Val Ile Ala Thr His		
119		210	215
120	Arg His Gly Lys Glu Thr Lys Ile His Ser Glu Ala Asn Lys Leu Lys		
121	225	230	235
122	His Asn Ile Arg Arg Ile Thr Gly Phe Glu Asn Arg Tyr Asp Phe Thr		
123		245	250
124	Gln Ile Pro His Arg Met Leu Leu Glu Asp Leu Leu Leu Ile Val Glu		
125		260	265
126	Asp Thr Cys Pro Thr Leu Asp Cys Thr Pro Arg Ala Arg Val Lys Leu		
127		275	280
128	Asn Arg Asp Asn Phe Pro Val Arg Thr Phe Pro Glu Tyr Thr Pro Glu		
129		290	295
130	Glu Arg Lys Gln Leu Glu Gln Ile Pro Tyr Arg Thr Glu Gln Leu Ser		
131	305	310	315
132	Ala Gln Glu Tyr Thr Gly Lys Asp Arg Ile Ala Pro Asn Pro Leu Asp		
133		325	330
134	Tyr Lys Ser Asn Ser Val Phe Met Lys Phe Gly Tyr His Phe Asn Ser		
135		340	345
136	Ser His Tyr Leu Gly Ala Ile Leu Glu Asp Thr Lys Thr Arg Tyr Asp		
137		355	360
138	Ile Arg Asp Met Gln Thr Pro Ala Tyr Tyr Thr Lys Asp Asp Ile Asn		
139		370	375
140	Leu Ser Leu Arg Asn Tyr Val Tyr Glu Gly Asp Asn Ile Leu Asp Gly		
141	385	390	395
142	Leu Val Phe Lys Pro Arg Ile Pro Tyr Gly Leu Arg Tyr Ser His Val		
143		405	410
144	Lys Phe Phe Asp Glu Arg His His Lys Arg Arg Leu Gly Phe Thr Tyr		
145		420	425
146	Lys Tyr Lys Pro Glu Asn Asn Arg Trp Leu Asp Ser Ile Lys Leu Ser		
147		435	440
148	Ala Asp Lys Gln Asp Ile Glu Leu Tyr Ser Arg Leu His Arg Leu His		
149		450	455
150	Cys Ser Asp Tyr Pro Val Asp Lys Asn Cys Arg Pro Thr Leu Asp		
151	465	470	475
152	Lys Ser Trp Ser Met Tyr Arg Thr Glu Arg Asn Asn Tyr Gln Glu Lys		
153		485	490
154	His Arg Val Ile His Leu Glu Phe Asp Lys Ala Leu Asn Ala Gly Gln		
155		500	505
156	Gly Val Phe Asn Gln Thr His Lys Leu Asn Leu Gly Leu Gly Phe Asp		
157		515	520

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158 Arg Phe Asn Ser Leu Met Asp His Gly Asp Met Thr Ala Gln Tyr Thr
159      530                      535                      540
160 Lys Gly Gly Tyr Thr Ser Tyr Arg Gly Arg Gly Arg Leu Asp Asn Pro
161 545                      550                      555                      560
162 Tyr Ile Tyr Arg Arg Asp Pro Arg Ser Ile Glu Thr Val Ser Leu Cys
163                      565                      570                      575
164 Asn Asn Thr Arg Gly Asp Ile Leu Asn Cys Glu Pro Arg Lys Ile Lys
165                      580                      585                      590
166 Gly Asp Ser His Phe Val Ser Phe Arg Asp Leu Val Ile Ser Glu Tyr
167                      595                      600                      605
168 Val Asp Leu Gly Leu Gly Val Arg Phe Asp Gln His Arg Phe Lys Ser
169      610                      615                      620
170 Asp Asp Pro Trp Thr Leu Ser Arg Thr Tyr Arg Asn Trp Ser Trp Asn
171 625                      630                      635                      640
172 Gly Gly Ile Thr Leu Lys Pro Thr Glu Phe Val Ser Leu Ser Tyr Arg
173                      645                      650                      655
174 Ile Ser Asn Gly Phe Arg Val Pro Ala Phe Tyr Glu Leu Tyr Gly Lys
175                      660                      665                      670
176 Arg Asp His Ile Gly Leu Lys Asp Asn Glu Tyr Val Gln Arg Ala Gln
177                      675                      680                      685
178 Arg Ser His Gln Leu Glu Pro Glu Lys Ser Thr Asn His Glu Ile Gly
179      690                      695                      700
180 Val Ser Phe Lys Gly Gln Phe Gly Tyr Leu Asp Val Ser Tyr Phe Arg
181 705                      710                      715                      720
182 Asn Asn Tyr Lys Asn Met Ile Ala Thr Ala Cys Lys Arg Ile Ile Gln
183                      725                      730                      735
184 Lys Ser His Cys Phe Tyr Asn Tyr His Asn Ile Gln Asp Val Ala Leu
185                      740                      745                      750
186 Asn Gly Ile Asn Leu Val Ala Lys Phe Asp Leu His Gly Ile Leu Ser
187                      755                      760                      765
188 Met Leu Pro Asp Gly Phe Tyr Ser Ser Val Ala Tyr Asn Arg Val Lys
189      770                      775                      780
190 Val Lys Glu Arg Lys Leu Thr Asp Ser Arg Leu Asp Ser Val Asn Asp
191 785                      790                      795                      800
192 Pro Ile Leu Asp Ala Ile Gln Pro Ala Arg Tyr Val Leu Gly Phe Gly
193                      805                      810                      815
194 Tyr Asp His Pro Glu Glu Lys Trp Gly Ile Gly Ile Thr Thr Thr Tyr
195                      820                      825                      830
196 Ser Lys Ala Lys Asn Ala Asp Glu Val Ala Gly Thr Arg His His Gly
197                      835                      840                      845
198 Ile His Arg Val Asp Leu Gly Gly Lys Leu Thr Gly Ser Trp Tyr Thr
199      850                      855                      860
200 His Asp Ile Thr Gly Tyr Ile Asn Tyr Lys Asn Tyr Thr Leu Arg Gly
201 865                      870                      875                      880
202 Gly Ile Tyr Asn Val Thr Asn Arg Lys Tyr Ser Thr Trp Glu Ser Val
203                      885                      890                      895
204 Arg Gln Ser Gly Val Asn Ala Val Asn Gln Asp Arg Gly Ser Asn Tyr
205                      900                      905                      910
206 Thr Arg Phe Gly Ala Pro Gly Arg Asn Phe Ser Leu Ala Phe Glu Met

```

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207          915          920          925
208 Lys Phe
209      930
212 <210> SEQ ID NO: 3
213 <211> LENGTH: 1755
214 <212> TYPE: DNA
215 <213> ORGANISM: Pasteurella haemolytica
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220 cccaaaaagc caagttttaca agatgataat agtaacgcaa gacgtacagt aagcgcttct 180
221 gaaactgaag ctttattgca gccgggggtt ggtttttcag ccaaaattcc gcgtcgtaat 240
222 ctcttccgc aggggaagga agatgtagcc cctattggtg atataaaaga gattactgga 300
223 gatctgccaa aaattccgta tgaagaagag gttaaagcgt gcggtagtag tgctgatgga 360
224 ttttagccata ctcatgatag aaatcataag ttgtatacaa gagattttaa ttttgttcgt 420
225 tccggctatg ttgtgcattc tgggtccaaa cctgaaataa agcctaaaga aattttgaga 480
226 acaggtgcac atgggtatgt ttactattta ggtatagagc cgcccaaagc aatacctacc 540
227 caaaaactaa cttataaagg atattgggat ttactacct atgcggctaa ggggagagat 600
228 agtaataattt ttctaattcc cgcaggcac aatagtggcg ccataccgga aaatagtcac 660
229 gatattaatg ttgatgattc tgaaaaacca atggggcata caggagaatt tacggctgat 720
230 tttgctaata aaactttaac tggaacattg gttcgtaatg ggtatgtag tcgtagcaaa 780
231 gagcaaaaaa ttacaacaat ttacgatatt gatgcgaaaa ttaaaggtaa tcgcttttct 840
232 ggtaaagcaa acccaaaaaa accgatgatc cttatttttg ggaaaagctc caccgacactt 900
233 gaaggtggat tttttggtgg ggaggtcaa gaacttgccg gtaaattctt agctgatgat 960
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235 gcctttgatg ctttcccaat taaacttaaa gatttaaata aatctgagat ggatactttc 1080
236 gggaaatgcga cacatttgat tattaacaat aagcagattc cacttattgc ggaagccaca 1140
237 aaaagctttg ccgagatgaa atttgatgat ttgggttacc gtactattga tggaaaaacg 1200
238 tatcgagttt cagtctgctg taataattta gattatgtca aatttgggat ttatagcgag 1260
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242 gatgtagatt ttgtcaataa aaaaattaat ggcaagctga ttgctaataa tgggtgttgaa 1500
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244 aaaacgggca attctggttt taatcttgat cccaaaagta cgaatgggtg cacggtaggg 1620
245 catataaata ctcaatttga agggggcttt tatggcccta aggcgacgga attaggtggt 1680
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249 <210> SEQ ID NO: 4
250 <211> LENGTH: 584
251 <212> TYPE: PRT
252 <213> ORGANISM: Pasteurella haemolytica
254 <400> SEQUENCE: 4
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257 Ala Ala Cys Ser Ser Asn Gly Gly Ser Phe Asp Val Gln Ser Ala Lys
258 20          25          30
259 Val Glu Ser Gln Thr Gln Thr Thr Pro Lys Lys Pro Ser Leu Gln Asp
260 35          40          45

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RAW SEQUENCE LISTING ERROR SUMMARY  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 2544  
Seq#:28; N Pos. 3,6,7,9,12,15  
Seq#:29; N Pos. 11,17,20  
Seq#:31; N Pos. 3,6,9,12